

SEQUENCE LISTING

<110> Helix Research Institute

<120> NOVEL GENES ASSOCIATED WITH THE MAINTENANCE  
OF DIFFERENTIATION OF SMOOTH MUSCLE CELLS

<130> H1-107PCT1

<140>

<141>

<150> JP 1999-248036

<151> 1999-07-29

<150> JP 2000-118776

<151> 2000-01-11

<150> JP 2000-183767

<151> 2000-05-02

<150> US 60/159590

<151> 1999-10-18

<150> US 60/183322

<151> 2000-02-17

1058549-01309

Ins  
A1

Ins  
A1

1

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30

Ins  
A1

130 \ 135 .140

Phe Ala Leu His Gly Ala His Val Ile Leu Ala Cys Arg Asn Met Ala

145                      150                      155

Arg Ala Ser Glu Ala Val Ser Arg Ile Leu Glu Glu Trp His Lys Ala

160                      165                      170                      175

Lys Val Glu Ala Met Thr Leu Asp Leu Ala Leu Leu Arg Ser Val Gln

180                  185                  190

cat ttt gct gaa gca ttc aag gcc aag aat gtg cct ctt cat gtg ctt 745

His Phe Ala Glu Ala Phe Lys Ala Lys Asn Val Pro Leu His Val Leu

195                      200                      205

gtg tgc aac gca gca act ttt gct cta|ccc tgg agt ctc acc aaa gat 793

Val Cys Asn Ala Ala Thr Phe Ala Leu ~~Pro~~ Trp Ser Leu Thr Lys Asp

210 215 220

ggc ctg gag acc acc ttt caa gtg aat cat ctg ggg cac ttc tac ctt 841

Gly Leu Glu Thr Thr Phe Gln Val Asn His ~~Leu~~ Gly His Phe Tyr Leu

225 230 235

Ins  
AI

Trp Val Tyr Thr Leu Leu Phe Thr Leu Ala Arg Pro Phe Thr Lys Ser

340

345

350

atg caa cag gga gct gcc acc acc gtg tac tgt gct gct gtc cca gaa 1225

Met Gln Gln Gly Ala Ala Thr Thr Val Tyr Cys Ala Ala Val Pro Glu

355

360

365

ctg gag ggt ctg gga ggg atg tac ttc aac aac tgc tgc cgc tgc atg 1273

Leu Glu Gly Leu Gly Gly Met Tyr Phe Asn Asn Cys Cys Arg Cys Met

370

375

380

ccc tca cca gaa gct cag agc gaa gag acg gcc cgg acc ctg tgg gcg 1321

Pro Ser Pro Glu Ala Gln Ser Glu Glu Thr Ala Arg Thr Leu Trp Ala

385

390

395

ctc agc gag agg ctg atc caa gaa cgg ctt ggc agc cag tcc ggc 1366

Leu Ser Glu Arg Leu Ile Gln Glu Arg Leu Gly Ser Gln Ser Gly

400

405

410

taagtggagc tcagagcgga tgggcacaca caccgcct gtgtgtgtcc cctcagcaa 1426

gtgccagggc tgggcccctt ccaaagtcc ctcaaaca gatccgcaag agtaaaggaa 1486

ataagagcag tcacaacaga gtgaaaaatc ttaagtacca atgggaagca gggaattcct 1546

ggggtaaagt atcacttttc tggggctggg ctaggcatag gtctctttgc tttctggtgg 1606

40069519-01223  
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taaaa accctgcttgg tgtgtag  
tcttt tactgtttata gaatagc  
accac tgcagccggg ggctggc  
ctcct tgcctgattg atccagg  
gctta gcaactgctg gggagac  
tgaca cccagaggga gtagaat  
tcctt tgctaattgct atgcaaa  
cctta gataccttga aaggcag  
ttggg gggcagagaa taaaacg  
ctctt gctttcacat tgtactt  
agaac atgcttgaat atcaaaa

<211> 414

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

Met Ala Ala Leu Arg Tyr Ala Gly Leu Asp Asp Thr Asp Ser Glu Asp

1

5

10

15

Glu Leu Pro Pro Gly Trp Glu Glu Arg Thr Thr Lys Asp Gly Trp Val

20

25

30

Tyr Tyr Ala Asn His Thr Glu Glu Lys Thr Gln Trp Glu His Pro Lys

35

40

45

Thr Gly Lys Arg Lys Arg Val Ala Gly Asp Leu Pro Tyr Gly Trp Glu

50

55

60

Gln Glu Thr Asp Glu Asn Gly Gln Val Phe Phe Val Asp His Ile Asn

65

70

75

80

Lys Arg Thr Thr Tyr Leu Asp Pro Arg Leu Ala Phe Thr Val Asp Asp

85

90

95

Asn Pro Thr Lys Pro Thr Thr Arg Gln Arg Tyr Asp Gly Ser Thr Thr

100

105

110

Ala Met Glu Ile Leu Gln Gly Pro Asp Phe Thr Gly Lys Val Val Val

40065518-012203  
 202210-01555004  
 Ins  
 A1



Ins  
AI

10/19

Val Val Ser Ser Glu Ser His Arg Phe Thr Asp Ile Asn Asp Ser Leu

260

265

270

Gly Lys Leu Asp Phe Ser Arg Leu Ser Pro Thr Lys Asn Asp Tyr Trp

275

280

285

Ala Met Leu Ala Tyr Asn Arg Ser Lys Leu Cys Asn Ile Leu Phe Ser

290

295

300

Asn Glu Leu His Arg Arg Leu Ser Pro Arg Gly Val Thr Ser Asn Ala

305

310

315

320

Val His Pro Gly Asn Met Met Tyr Ser Asn Ile His Arg Ser Trp Trp

325

330

335

Val Tyr Thr Leu Leu Phe Thr Leu Ala Arg Pro Phe Thr Lys Ser Met

340

345

350

Gln Gln Gly Ala Ala Thr Thr Val Tyr Cys Ala Ala Val Pro Glu Leu

355

360

365

Glu Gly Leu Gly Gly Met Tyr Phe Asn Asn Cys Cys Arg Cys Met Pro

370

375

380

Ser Pro Glu Ala Gln Ser Glu Glu Thr Ala Arg Thr Leu Trp Ala Leu

385

390

395

400

203240635004  
Ins  
A1

Ser Glu Arg Leu Ile Gln Glu Arg Leu Gly Ser Gln Ser Gly

405

410

&lt;210&gt; 3

&lt;211&gt; 251

&lt;212&gt; DNA

&lt;213&gt; Gallus gallus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (3).. (251)

&lt;400&gt; 3

ag gag cgc acc acc aag gac ggc tgg gtt tac tac gcc aat cac ttg 47

Glu Arg Thr Thr Lys Asp Gly Trp Val Tyr Tyr Ala Asn His Leu

1

5

10

15

gaa gaa aaa aca cag tgg gaa cat cca aaa tct ggg aag agg aaa cgt 95

Glu Glu Lys Thr Gln Trp Glu His Pro Lys Ser Gly Lys Arg Lys Arg

20

25

30

gtt gca gga ggt ctg cca tat gga tgg gag cag gag act gat gaa aat 143

Val Ala Gly Gly Leu Pro Tyr Gly Trp Glu Gln Glu Thr Asp Glu Asn

35

40

45

203210255001  
Ins  
A1

gga cag gtc tat ttt gta gac cac ata aac aaa aga act acc tat ctg 191  
 Gly Gln Val Tyr Phe Val Asp His Ile Asn Lys Arg Thr Thr Tyr Leu  
                   50                                  55                                  60

gat cca aga ttg gcc ttt aca gtt gaa gat aat cca gca aag cca cct 239  
 Asp Pro Arg Leu Ala Phe Thr Val Glu Asp Asn Pro Ala Lys Pro Pro  
                   65                                  70                                  75

act aga caa aaa 251  
 Thr Arg Gln Lys  
                   80

<210> 4

<211> 83

<212> PRT

<213> Gallus gallus

<400> 4

Glu Arg Thr Thr Lys Asp Gly Trp Val Tyr Tyr Ala Asn His Leu Glu  
           1                                  5                                  10                                  15

Glu Lys Thr Gln Trp Glu His Pro Lys Ser Gly Lys Arg Lys Arg Val  
                                   20                                  25                                  30

203666039303  
 Ins  
 A1

35                      40                      45

50                      55                      60

65                      70 \                      75                      80

Ins  
A1

<211> 30

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<223> Description of Artificial Sequence:Artificially  
Synthesized Sequence

agcaucgagu cggccuuguu ggccuacugg

<210> 6

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
Synthesized Primer Sequence

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gcggctgaag acggcctatg tggccttttt ttttttttt tt

42

<210> 7

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
Synthesized Primer Sequence

<400> 7

agcatcgagt cggccttggt g

21

Ins  
A1

<210> 8

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
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<400> 8

gcggctgaag acggcctatg t

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<210> 9

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially  
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gcaggaacat ggcaaggcg agtg

24

Ins  
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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially  
Synthesized Primer Sequence

<400> 10

gggcaggagc tgagcggcac aaa

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<210> 11

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
Synthesized Primer Sequence

<400> 11

ggtggctttg ctggattatc tt

22

4056549-04299

Ins  
AI



Ins  
Al

7

~~<210> 12~~  
~~<211> 22~~  
~~<212> DNA~~  
~~<213> Artificial Sequence~~

 $\langle 220 \rangle$ 

<223> Description of Artificial Sequence:Artificially  
Synthesized Primer Sequence

<223> Description of Artificial Sequence:Artificially  
Synthesized Primer Sequence

gttgcaggag gtcctgccata tg

22

<211> 20

## <212> DNA

### <213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> Description of Artificial Sequence:Artificially  
Synthesized Primer Sequence

<223> Description of Artificial Sequence:Artificially  
Synthesized Primer Sequence

tacggaagtg ttacttctgc

20



<210> 16

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
Synthesized Primer Sequence

<400> 16

caggaaacag ctatgac

Ins  
A1

20221018155500